

135

(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau



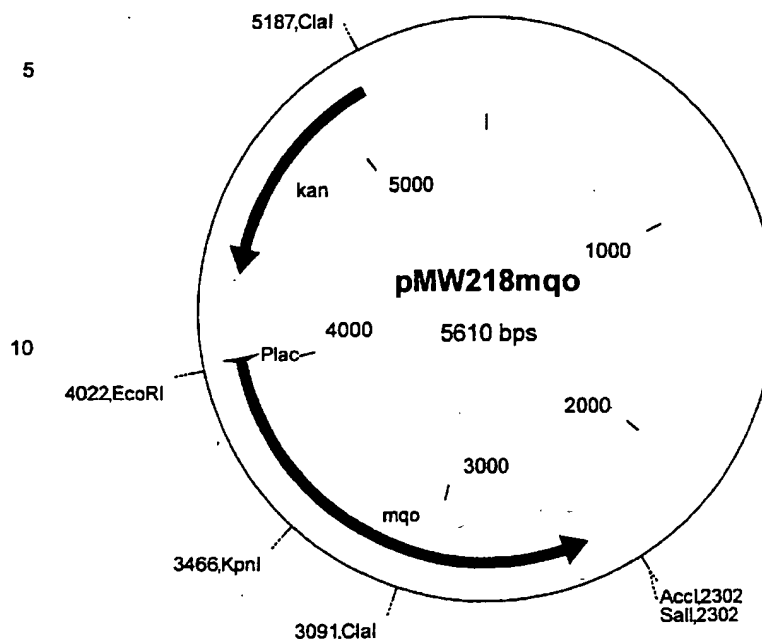
(43) International Publication Date
24 January 2002 (24.01.2002)

PCT

(10) International Publication Number
WO 02/06459 A1

- (51) International Patent Classification⁷: C12N 9/02, MOLENAAR, Douwe; Hofstrasse 12, Baesweiler 52499 (DE).
C12P 13/08, C12N 15/53
- (21) International Application Number: PCT/EP01/05548 (81) Designated States (*national*): AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CR, CU, CZ, DE, DK, DM, DZ, EE, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, TZ, UA, UG, UZ, VN, YU, ZA, ZW.
- (22) International Filing Date: 16 May 2001 (16.05.2001)
- (25) Filing Language: English
- (26) Publication Language: English
- (30) Priority Data:
100 34 833.5 18 July 2000 (18.07.2000) DE
101 03 874.7 30 January 2001 (30.01.2001) DE
- (84) Designated States (*regional*): ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).
- (71) Applicant: DEGUSSA AG [DE/DE]; Bennigsenplatz 1, 40474 Düsseldorf (DE).
- Published:
— with international search report
- (72) Inventors: RIEPING, Mechthild; Mönkebergstrasse 1, 33619 Bielefeld (DE). THIERBACH, Georg; Gunststrasse 21, 33613 Bielefeld (DE). VAN DER REST, Michel, Eduard; Akkerwinde 24A, NL-5913 Venlo (NL).
- For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: PROCESS FOR THE FERMENTATIVE PREPARATION OF L-THREONINE



(57) Abstract: The invention provides a process for the fermentative preparation of L-threonine using Enterobacteriaceae which in particular already produce L-threonine and in which the nucleotide sequence(s) which code(s) for the mqo gene are enhanced, in particular over-expressed.



WO 02/06459 A1

Process for the fermentative preparation of L-threonine

This invention relates to the new amino acid sequence of the malate:quinone oxidoreductase enzyme protein (Mqo) of Enterobacteriaceae and to a process for the fermentative
5 preparation of L-threonine using Enterobacteriaceae in which the mqo gene is enhanced.

Prior Art

L-Threonine is used in animal nutrition, in human medicine and in the pharmaceuticals industry. It is known that L-
10 threonine can be prepared by fermentation of strains of Enterobacteriaceae, in particular Escherichia coli and Serratia marcescens. Because of their great importance, work is constantly being undertaken to improve the preparation processes. Improvements to the process can
15 relate to fermentation measures, such as e.g. stirring and supply of oxygen, or the composition of the nutrient media, such as e.g. the sugar concentration during the fermentation, or the working up to the product form by e.g. ion exchange chromatography, or the intrinsic output
20 properties of the microorganism itself.

Methods of mutagenesis, selection and mutant selection are used to improve the output properties of these microorganisms. Strains which are resistant to
antimetabolites, such as e.g. the threonine analogue α -
25 amino- β -hydroxyvaleric acid (AHV), or are auxotrophic for metabolites of regulatory importance and produce L-threonine are obtained in this manner.

Methods of the recombinant DNA technique have also been employed for some years for improving the strain of
30 Enterobacteriaceae strains which produce L-threonine, by amplifying individual threonine biosynthesis genes and investigating the effect on the L-threonine production.

Object of the Invention

The inventors had the object of providing new measures for improved fermentative preparation of L-threonine.

Description of the Invention

- 5 The invention provides a polypeptide from Enterobacteriaceae with malate:quinone oxidoreductase (Mqo) activity (E.C. 1.1.99.16) chosen from the group consisting of
- 10 a) polypeptide with the amino acid sequence shown in SEQ ID NO. 2, or
- b) polypeptide which is at least 70%, preferably at least 80%, particularly preferably at least 90 to 95% identical to the amino acid sequence shown in SEQ ID NO. 2, or
- 15 c) polypeptide according to SEQ ID NO. 2, including deletion, insertion or exchange of one or more amino acids, or
- d) polypeptide according to SEQ ID NO. 2, including N- or C-terminal lengthening by one or more amino acids,
- 20 the total length of the polypeptide according to b), c) or d) being at least 514 and at most 544, preferably at least 519 and at most 539, in a preferred form at least 524 and at most 534, particularly preferably at least 527 and at most 531 amino acid radicals.
- 25 The invention furthermore provides a polynucleotide from Enterobacteriaceae which codes for a polypeptide with malate:quinone oxidoreductase (Mqo) activity (E.C. 1.1.99.16), chosen from the group consisting of

- a) DNA which contains the nucleotide sequence corresponding to nucleobases 7 to 1593 of SEQ ID NO. 1, or
- b) DNA according to a) corresponding to the degeneration of the genetic code, or
- c) DNA according to a) containing sense mutations of neutral function, or
- d) DNA which is at least 70%, preferably at least 80%, particularly preferably at least 90 to 95% identical to that mentioned in a) or b), or
- e) polynucleotide which hybridizes with the DNA according to a), b), c) or d).

The invention also provides

- a DNA which is capable of replication and codes for the polypeptide shown in SEQ ID NO. 2,
- a vector containing the mqo gene corresponding to nucleobases 7 to 1593 of SEQ ID NO. 1, in particular plasmid pMW218mqo shown in figure 1.

"Polynucleotide" in general relates to polyribonucleotides and polydeoxyribonucleotides, it being possible for these to be non-modified RNA or DNA or modified RNA or DNA.

"Polypeptides" is understood as meaning peptides or proteins which comprise two or more amino acids bonded via peptide bonds.

- The polypeptides according to the invention include the polypeptides according to SEQ ID NO. 2, which have malate:quinone oxidoreductase activity, and also those which are at least 70%, preferably at least 80% and in particular at least 90% to 95% identical to the polypeptide according to SEQ ID NO. 2 and have the activity mentioned.

Finally, the invention provides a process for the fermentative preparation of L-threonine using Enterobacteriaceae which in particular already produce L-threonine and in which the nucleotide sequence(s) which
5 code(s) for the mqo gene are enhanced, in particular over-expressed.

In particular, the process is a process for the preparation of L-threonine, which comprises carrying out the following steps:

- 10 a) fermentation of microorganisms of the family Enterobacteriaceae in which at least the mqo gene is enhanced (over-expressed), optionally in combination with further genes,
- 15 b) concentration of the L-threonine in the medium or in the cells of the microorganisms of the family Enterobacteriaceae, and
- c) isolation of the L-threonine.

The term "enhancement" in this connection describes the increase in the intracellular activity of one or more
20 enzymes or proteins in a microorganism which are coded by the corresponding DNA, for example by increasing the number of copies of the gene or genes, using a potent promoter or a gene which codes for a corresponding enzyme or protein with a high activity, and optionally combining these
25 measures.

The microorganisms which the present invention provides can prepare L-threonine from glucose, sucrose, lactose, fructose, maltose, molasses, starch, or from glycerol and ethanol. They are representatives of Enterobacteriaceae,
30 in particular of the genera Escherichia and Serratia. Of the genus Escherichia the species E. coli and of the genus Serratia the species Serratia marcescens are to be mentioned in particular.

Suitable L-threonine-producing strains of the genus *Escherichia*, in particular of the species *E. coli*, are, for example

- 5 *Escherichia coli* TF427
- Escherichia coli* H4578
- Escherichia coli* KY10935
- Escherichia coli* EL1003
- Escherichia coli* VNIIGenetika MG-442
- Escherichia coli* VNIIGenetika VL334/pYN7
- 10 *Escherichia coli* VNIIGenetika M1
- Escherichia coli* VNIIGenetika 472T23
- Escherichia coli* VNIIGenetika TDH-6
- Escherichia coli* BKIIM B-3996
- Escherichia coli* BKIIM B-5318
- 15 *Escherichia coli* B-3996-C43
- Escherichia coli* B-3996-C80
- Escherichia coli* B-3996/pTWV-pps
- Escherichia coli* B-3996(pMW::THY)
- Escherichia coli* B-3996/pBP5
- 20 *Escherichia coli* kat 13
- Escherichia coli* KCCM-10132

Suitable L-threonine-producing strains of the genus *Serratia*, in particular of the species *Serratia marcescens*, are, for example

- 25 *Serratia marcescens* HNr21
- Serratia marcescens* TLr156
- Serratia marcescens* T2000.

The nucleotide sequence of the chromosome of *E. coli* is known and is available in databanks accessible to the
30 public, such as, for example, the databank of the European Molecular Biology Laboratories (EMBL, Heidelberg, Germany).

Examples of such sequences deposited are the entries accessible under number AE000310 or D90850.

In the work on the present invention it was possible to identify the mgo gene, which codes for malate:quinone
5 oxidoreductase, of E. coli (SEQ ID NO. 1) and the amino acid sequence of the Mgo enzyme protein formed (SEQ ID NO. 2).

It has furthermore been possible to isolate two further new malate:quinone oxidoreductase proteins, designated protein B
10 and C, which have the N-terminal amino acid sequence shown in SEQ ID No. 11 and 12. These are also provided by the invention.

It has been found that Enterobacteriaceae produce L-threonine in an improved manner after over-expression of
15 the mgo gene, which codes for malate:quinone oxidoreductase (E.C. 1.1.99.16).

According to the invention, it is also possible to use a DNA section which contains the DNA sequence of the gene of the malate:quinone oxidoreductase given in the databank of
20 the National Center for Biotechnology Information (NCBI, Bethesda, MD, USA) with accession number P33940.

Alleles of the mgo gene which result from the degeneracy of the genetic code or due to "sense mutations" of neutral function can furthermore be used. It is also known that
25 the amino acid methionine or formylmethionine coded by the start codon ATG can be removed in various proteins by enzymes of the host.

To achieve an over-expression, the number of copies of the corresponding genes can be increased, or the promoter and
30 regulation region or the ribosome binding site upstream of the structural gene can be mutated. Expression cassettes which are incorporated upstream of the structural gene act in the same way. By inducible promoters, it is

additionally possible to increase the expression in the course of fermentative L-threonine production. The expression is likewise improved by measures to prolong the life of the m-RNA. Furthermore, the enzyme activity is
5 also increased by preventing the degradation of the enzyme protein. The genes or gene constructions can either be present in plasmids with a varying number of copies, or can be integrated and amplified in the chromosome.
Alternatively, an over-expression of the genes in question
10 can furthermore be achieved by changing the composition of the media and the culture procedure.

Instructions in this context can be found by the expert, inter alia, in Chang and Cohen (Journal of Bacteriology 134:1141-1156 (1978)), in Hartley and Gregori (Gene 13:347-
15 353 (1981)), in Amann and Brosius (Gene 40:183-190 (1985)), in de Broer et al. (Proceedings of the National (sic) of Sciences of the United States of America 80:21-25 (1983)), in LaVallie et al. (BIO/TECHNOLOGY 11, 187-193 (1993)), in WO 98/04715, in Llosa et al. (Plasmid 26:222-224 (1991)),
20 in Quandt and Klipp (Gene 80:161-169 (1989)), in Hamilton (Journal of Bacteriology 171:4617-4622 (1989)), in Jensen and Hammer (Biotechnology and Bioengineering 58, 191-195 (1998) and in known textbooks of genetics and molecular biology.

25 Plasmid vectors which are capable of replication in Enterobacteriaceae, such as e.g. cloning vectors derived from pACYC184 (Bartolomé et al.; Gene 102, 75-78 (1991)), pTrc99A, which is described by Amann et al. (Gene 69:301-315 (1988)), or pSC101 derivatives (Vocke and Bastia,
30 Proceedings of the National Academy of Science, USA 80 (21):6557-6561 (1983)) can be used. A strain transformed with a plasmid vector where the plasmid vector carries the nucleotide sequence which codes for the mqo gene can be employed in a process according to the invention.

In addition, it may be advantageous for the production of L-threonine with strains of the family Enterobacteriaceae to enhance, in particular to over-express, one or more enzymes of the known threonine biosynthesis pathway or
5 enzymes of anaplerotic metabolism or enzymes for the production of reduced nicotinamide adenine dinucleotide phosphate, in addition to the *mgo* gene.

Thus, for example, one or more genes chosen from the group consisting of

- 10 • the *thrABC* operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase (US-A-4,278,765),
- the *pyc* gene which codes for pyruvate carboxylase (DE-A-19 831 609),
- 15 • the *pps* gene which codes for phosphoenol pyruvate synthase (Molecular and General Genetics 231:332 (1992)),
- the *ppc* gene which codes for phosphoenol pyruvate carboxylase (Gene 31:279-283 (1984)),
- 20 • the genes *pntA* and *pntB* which code for transhydrogenase (European Journal of Biochemistry 158:647-653 (1986)),
- the *rhtB* gene which imparts homoserine resistance (EP-A-0994190)
- the *rhtC* gene which imparts threonine resistance
25 (EP-A-1013765), and
- the *gdhA* gene which codes for glutamate dehydrogenase (Gene 27:193-199 (1984))

can be enhanced, in particular over-expressed, at the same time.

It may furthermore be advantageous for the production of L-threonine, in addition to the enhancement of the mqo gene, for one or more of the genes chosen from the group consisting of:

- 5 • the tdh gene which codes for threonine dehydrogenase (Ravnikar and Somerville, Journal of Bacteriology 169, 4716-4721 (1987)),
- the mdh gene which codes for malate dehydrogenase (E.C. 1.1.1.37)

- 10 to be attenuated, in particular to be eliminated or for the expression thereof to be reduced at the same time.

Finally, in addition to enhancement of the mqo gene it may be advantageous for the production of L-threonine to eliminate undesirable side reactions, (Nakayama: "Breeding
15 of Amino Acid Producing Microorganisms", in: Overproduction of Microbial Products, Krumphanzl, Sikyta, Vanek (eds.), Academic Press, London, UK, 1982). Bacteria in which the metabolic pathways which reduce the formation of L-threonine are at least partly eliminated can be employed in
20 a process according to the invention.

The microorganisms produced according to the invention can be cultured in the batch process (batch culture) or in the fed batch process (feed process). A summary of known culture methods is described in the textbook by Chmiel
25 (Bioprozesstechnik 1. Einführung in die Bioverfahrenstechnik [Bioprocess Technology 1. Introduction to Bioprocess Technology (Gustav Fischer Verlag, Stuttgart, 1991)) or in the textbook by Storhas (Bioreaktoren und periphere Einrichtungen [Bioreactors and Peripheral
30 Equipment] (Vieweg Verlag, Braunschweig/Wiesbaden, 1994)).

The culture medium to be used must meet the requirements of the particular strains in a suitable manner. Descriptions of culture media for various microorganisms are contained

in the handbook "Manual of Methods for General Bacteriology" of the American Society for Bacteriology (Washington D.C., USA, 1981).

Sugars and carbohydrates, such as e.g. glucose, sucrose,
5 lactose, fructose, maltose, molasses, starch and optionally cellulose, oils and fats, such as e.g. soya oil, sunflower oil, groundnut oil and coconut fat, fatty acids, such as e.g. palmitic acid, stearic acid and linoleic acid, alcohols, such as e.g. glycerol and ethanol, and organic
10 acids, such as e.g. acetic acid, can be used as the source of carbon. These substances can be used individually or as a mixture.

Organic nitrogen-containing compounds, such as peptones, yeast extract, meat extract, malt extract, corn steep
15 liquor, soya bean flour and urea, or inorganic compounds, such as ammonium sulphate, ammonium chloride, ammonium phosphate, ammonium carbonate and ammonium nitrate, can be used as the source of nitrogen. The sources of nitrogen can be used individually or as a mixture.

20 Phosphoric acid, potassium dihydrogen phosphate or dipotassium hydrogen phosphate or the corresponding sodium-containing salts can be used as the source of phosphorus. The culture medium must furthermore comprise salts of metals, such as e.g. magnesium sulfate or iron sulfate,
25 which are necessary for growth. Finally, essential growth substances, such as amino acids and vitamins, can be employed in addition to the abovementioned substances. Suitable precursors can moreover be added to the culture medium. The starting substances mentioned can be added to
30 the culture in the form of a single batch, or can be fed in during the culture in a suitable manner.

Basic compounds, such as sodium hydroxide, potassium hydroxide, ammonia or aqueous ammonia, or acid compounds, such as phosphoric acid or sulfuric acid, can be employed

in a suitable manner to control the pH. Antifoams, such as e.g. fatty acid polyglycol esters, can be employed to control the development of foam. Suitable substances having a selective action, e.g. antibiotics, can be added
5 to the medium to maintain the stability of plasmids. To maintain aerobic conditions, oxygen or oxygen-containing gas mixtures, such as e.g. air, are introduced into the culture. The temperature of the culture is usually 25°C to 45°C, and preferably 30°C to 40°C. Culturing is continued
10 until a maximum of L-threonine has formed. This target is usually reached within 10 hours to 160 hours.

The analysis of L-threonine can be carried out by anion exchange chromatography with subsequent ninhydrin derivatization, as described by Spackman et al. (Analytical
15 Chemistry, 30, (1958), 1190), or it can take place by reversed phase HPLC as described by Lindroth et al. (Analytical Chemistry (1979) 51: 1167-1174).

A pure culture of the L-threonine-producing strain B-3996kur Δ tdh/pVIC40, pMW218mqo was deposited on 24th
20 January 2001 at the Deutsche Sammlung für Mikroorganismen und Zellkulturen (DSMZ = German Collection of Microorganisms and Cell Cultures, Braunschweig, Germany) as DSM 14004.

The process according to the invention is used for the
25 fermentative preparation of amino acids, in particular L-threonine and L-isoleucine.

The present invention is explained in more detail in the following with the aid of embodiment examples.

The isolation of plasmid DNA from E. coli and all
30 techniques of restriction, Klenow and alkaline phosphatase treatment are carried out by the method of Sambrook et al. (Molecular cloning - A laboratory manual (1989) Cold Spring Harbour Laboratory Press). Unless described otherwise, the

transformation of *E. coli* is carried out by the method of Chung et al. (Proceedings of the National Academy of Sciences of the United States of America USA (1989) 86:2172-2175).

- 5 The incubation temperature during preparation of strains and transformants is 37°C. Temperatures of 30°C and 44°C are used in the gene replacement process according to Hamilton et.al.

Example 1.

- 10 Construction of the expression plasmid pMW218mqo

The mqo gene from *E. coli* K12 is amplified using the polymerase chain reaction (PCR) and synthetic oligonucleotides. Starting from the nucleotide sequence of the yojH gene in *E. coli* K12 MG1655 (EMBL AE000310), PCR

- 15 primers (see SEQ ID No. 3 and 4) are synthesized (MWG Biotech, Ebersberg, Germany):

YojH1: 5' - GCGGAATTCGATGGCGGCAAAAGCG - 3'

YojH2: 5' - GTTACGCCGCATCCAACATC - 3'

- The chromosomal *E. coli* K12 MG1655 DNA employed for the PCR
20 is isolated according to the manufacturers instructions with "QIAGEN Genomic-tips 100/G" (QIAGEN, Hilden, Germany). A DNA fragment approx. 1700 base pairs (bp) in size can be amplified with the specific primers under standard PCR conditions (Innis et al. (1990) PCR protocols. A guide to
25 methods and applications, Academic Press) with Pfu-DNA polymerase (Promega Corporation, Madison, USA). The PCR product is cleaved with the enzyme EcoRI and ligated with the plasmid pMW218 (Nippon Gene, Toyama, Japan), which is cleaved with the enzymes EcoRI and SmaI. The *E. coli*
30 strain DH5α is transformed with the ligation batch and plasmid-carrying cells are selected on LB agar (Lennox, Virology 1:190 (1955)), to which 20 µg/ml kanamycin is

added. Successful cloning of the mqo gene can be demonstrated after plasmid DNA isolation and control cleavage with EcoRI, AccI and ClaI. The plasmid is designated pMW218mqo (figure 1).

5 Example 2

Preparation of L-threonine with the strain MG442/pMW218mqo

2.1 Preparation of the strain MG442/pMW218mqo

The L-threonine-producing E. coli strain MG442 is described in US-A- 4,278,765 and deposited as CMIM.B-1628 at the
10 Russian National Collection for Industrial Microorganisms (VKPM, Moscow, Russia).

The strain MG442 is transformed with the plasmid pMW218mqo and plasmid-carrying cells are selected on LB agar supplemented with 20 µg/ml kanamycin. The strain is
15 designated MG442/pMW218mqo.

2.2 Preparation of L-threonine

Selected individual colonies of MG442/pMW218mqo are multiplied further on minimal medium with the following composition: 3.5 g/l $\text{Na}_2\text{HPO}_4 \cdot 2\text{H}_2\text{O}$, 1.5 g/l KH_2PO_4 , 1 g/l
20 NH_4Cl , 0.1 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 25 mg/l isoleucine, 2 g/l glucose, 20 g/l agar, 20 mg/l kanamycin. The formation of L-threonine is checked in batch cultures of 10 ml contained in 100 ml conical flasks. For this, 10 ml of preculture medium of the following composition: 2 g/l yeast extract,
25 10 g/l $(\text{NH}_4)_2\text{SO}_4$, 1 g/l KH_2PO_4 , 0.5 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 15 g/l CaCO_3 , 20 g/l glucose, 20 mg/l kanamycin are inoculated and the batch is incubated for 16 hours at 37°C and 180 rpm on an ESR incubator from Kühner AG (Birsfelden, Switzerland). In each case 250 µl of this preculture are transinoculated
30 into 10 ml of production medium (25 g/l $(\text{NH}_4)_2\text{SO}_4$, 2 g/l KH_2PO_4 , 1 g/l $\text{MgSO}_4 \cdot 7\text{H}_2\text{O}$, 0.03 g/l $\text{FeSO}_4 \cdot 7\text{H}_2\text{O}$, 0.018 g/l $\text{MnSO}_4 \cdot \text{H}_2\text{O}$, 25 mg/l isoleucine, 30 g/l CaCO_3 , 20 g/l

glucose) and the batch is incubated for 48 hours at 37°C. After the incubation the optical density (OD) of the culture suspension is determined with an LP2W photometer from the company Dr. Lange (Berlin, Germany) at a measurement wavelength of 660 nm.

The concentration of L-threonine formed is then determined in the sterile-filtered culture supernatant with an amino acid analyzer from Eppendorf-BioTronik (Hamburg, Germany) by ion exchange chromatography and post-column reaction with ninhydrin detection.

The result of the experiment is shown in Table 1.

Table 1

Strain	OD (660 nm)	L-Threonine g/l
MG442	4.7	0.46
MG442/pMW218mqo	4.5	0.89

Example 3

15 Preparation of L-threonine with the strain
B-3996kurΔtdh/pVIC40, pMW218mqo

The L-threonine-producing E. coli strain B-3996 is described in US-A- 5,175,107 and deposited at the Russian National Collection for Industrial Microorganisms (VKPM, Moscow, Russia).

3.1 Preparation of the strain B-3996kurΔtdh/pVIC40,
pMW218mqo

After culture in antibiotic-free complete medium for approximately ten generations, a derivative of strain B-3996 which no longer contains the plasmid pVIC40 is

isolated. The strain formed is streptomycin-sensitive and is designated B-3996kur.

The method described by Hamilton et al. (Journal of Bacteriology (1989) 171: 4617-4622), which is based on the use of the plasmid pMAK705 with a temperature-sensitive replicon, is used for incorporation of a deletion into the *tdh* gene. The plasmid pDR121 (Ravnikar and Somerville, Journal of Bacteriology (1987) 169:4716-4721) contains a DNA fragment from *E. coli* 3.7 kilo-base pairs (kbp) in size, on which the *tdh* gene is coded. To generate a deletion of the *tdh* gene region, pDR121 is cleaved with the restriction enzymes *Cla*I and *Eco*RV and the DNA fragment 5 kbp in size isolated is ligated, after treatment with Klenow enzyme. The ligation batch is transformed in the *E. coli* strain DH5 α and plasmid-carrying cells are selected on LB agar, to which 50 μ g/ml ampicillin are added.

Successful deletion of the *tdh* gene can be demonstrated after plasmid DNA isolation and control cleavage with *Eco*RI. The *Eco*RI fragment 1.7 kbp in size is isolated, and ligated with the plasmid pMAK705, which is partly digested with *Eco*RI. The ligation batch is transformed in DH5 α and plasmid-carrying cells are selected on LB agar, to which 20 μ g/ml chloramphenicol are added. Successful cloning is demonstrated after isolation of the plasmid DNA and cleavage with *Eco*RI. The pMAK705 derivative formed is designated pDM32.

For the gene replacement, B-3996kur is transformed with the plasmid pDM32. The replacement of the chromosomal *tdh* gene with the plasmid-coded deletion construct is carried out by the selection process described by Hamilton et al. and is verified by standard PCR methods (Innis et al. (1990), PCR Protocols. A Guide to Methods and Applications, Academic Press) with the following oligonucleotide primers (see SEQ ID No. 5 and 6).

Tdh1: 5'-TCGCGACCTATAAGTTTGGG-3'

Tdh2: 5'-AATACCAGCCCTTGTTCTGTG-3'.

The strain formed is tested for kanamycin sensitivity and is designated B-3996kur Δ tdh.

- 5 B-3996kur Δ tdh is transformed with the plasmid pVIC40 isolated from B-3996 and plasmid-carrying cells are selected on LB agar with 20 μ g/ml streptomycin. A selected individual colony is designated B-3996kur Δ tdh/pVIC40 and transformed with the plasmid pMW218mqo. Selection is
10 carried out on LB-agar to which 20 μ g/ml streptomycin and 50 μ g/ml kanamycin are added. The strain formed in this way is designated B-3996kur Δ tdh/pVIC40, pMW218mqo.

3.2 Preparation of L-threonine

The preparation of L-threonine by the strains

- 15 B-3996kur Δ tdh/pVIC40 and B-3996kur Δ tdh/pVIC40, pMW218mqo is tested as described in example 2, the minimal medium and the production medium not being supplemented with L-isoleucine. The minimal medium, the preculture medium and the production medium are supplemented with 20 μ g/ml
20 streptomycin for B-3996kur Δ tdh/pVIC40 and with 20 μ g/ml streptomycin and 50 μ g/ml kanamycin for B-3996kur Δ tdh/pVIC40, pMW218mqo.

The result of the experiment is summarized in Table 2.

Table 2

Strain	OD (660 nm)	L- Threonine
B-3996kur Δ tdh/pVIC40	4.7	6.26
B-3996kur Δ tdh/pVIC40, pMW218mqo	3.7	7.72

Example 4

Preparation of a vector containing a histidine-tagged malate:quinone oxidoreductase gene of E. coli

A 1744 bp DNA fragment, which codes for the malate:quinone
5 oxidoreductase protein extended by a six-fold histidine radical on the C-terminal end, was prepared by means of the polymerase chain reaction (PCR) and then cloned.

The primer YOJH1a (SEQ ID No 7) was drafted with the aid of the known nucleotide sequence with Accession Number
10 AE000310 (EMBL, European Molecular Biology Laboratories, Heidelberg, Germany). This primer has the sequence:

5'-GGA TCC GTT GAT GCC GCG CAA ATC-3'.

The primer YCHIS (SEQ ID No 8), which has the following sequence, was employed as the second primer:

15 5'-CGC GAA TTC TTA GTG GTG GTG GTG GTG CAA CGC AAT ATC CGC CAC-3'.

The primers shown were synthesized by MWG Biotech (Ebersberg, Germany). The PCR reaction was carried out by the standard PCR method of Innis et al., (PCR Protocols. A
20 Guide to Methods and Applications, 1990, Academic Press, New York, USA).

Whole DNA isolated from a colony of the E. coli strain MC4100 (Casadaban et al. Journal of Molecular Biology 104, 541-555, 1976) served as the template.

25 The PCR was carried out in a Thermocycler from Techne (Cambridge, UK). The samples were first denatured for 5 minutes at 94°C and the Taq polymerase from Promega (Madison, WI, USA) was then added to the sample batch. A cycle comprising denaturing (60 seconds, 94°C), annealing
30 (60 seconds, 60°C) and synthesis (120 seconds, 72°C) was then passed through 10 times, the annealing temperature

being increased by 0.4°C in each cycle. The subsequent 25 cycles comprised denaturing (60 seconds, 94°C), annealing (60 seconds, 64°C) and synthesis (120 seconds, 72°C). Finally, a concluding synthesis of 10 minutes at 72°C was
5 carried out.

The DNA fragment 1744 bp in length containing the mqo gene amplified in this manner was purified with the aid of the QIAQuick PCR Purification Kit from Qiagen (Hilden, Germany) and then digested with the restriction enzymes BamHI and
10 EcoRI. These restriction cleavage sites were generated during the PCR with the aid of the primers YOJHI and YCHIS. After gel electrophoresis, the digested DNA fragment was cut out of the agarose gel and purified with QIAEX II Gel Extraction Kit (155) (Hilden, Germany), mixed into the
15 vector pUC19 treated with the restriction enzymes BamHI and EcoRI (Yanisch-Perron et al., Gene 33, 103-119, 1985) and then treated with T4 DNA ligase.

An E. coli strain designated MC4100Δmqo, which contains a deletion in the mqo gene and was prepared according to the
20 prior art, was used as the cloning host for the transformation. For this, the mqo gene was first amplified with the aid of the primers Y_01 (SEQ ID No 9) and Y_04 (SEQ ID No 10) using whole DNA isolated from strain MC4100, with the aid of the PCR method. The PCR conditions
25 comprised 30 cycles of denaturing (30 seconds, 94°C), annealing (30 seconds, 60°C) and synthesis (2 minutes, 72°C).

The primer Y_01 has the following sequence:
5'-GCTGGATGAATGGGCGGCGG-3'

30 The primer Y_04 has the following sequence:
5'-CGCGGATCCCCGGTTTCAACGATGATG-3'

The amplified DNA fragment contains a cleavage site for the restriction enzyme BamHI directly after the primer Y_01.

The BamHI restriction cleavage site contained in the oligonucleotide primer Y_04 is identified by underlining. The amplified DNA fragment was digested with BamHI and then incorporated into the BamHI cleavage site of the plasmid pKO3mqo described by Link et al. (Journal of Bacteriology 179, 6228-6237 (1997)). The resulting plasmid was designated pKO3mqo and treated with the restriction enzyme MluI in order to remove an internal DNA segment of the mqo gene 416 bp long (deletion). The plasmid pKO3 Δ mqo obtained in this manner was used for incorporation of the deletion Δ mqo in the strain MC4100. The method described by Link et al (Journal of Bacteriology 179, 6228-6237 (1997)) was employed for this.

The strain MC4100 Δ mqo was transformed with the ligation mixture described above. Transformants were selected on LB medium, which had been supplemented with 100 μ g/ml carbenicillin. A plasmid was isolated from a transformant and designated pUCH2. Plasmid pUCH2 contains a DNA fragment 1744 bp long, which codes for the malate:quinone oxidoreductase protein extended by a six-fold histidine radical on the C-terminal end.

Example 5

Isolation and purification of the over-expressed histidine-tagged malate:quinone oxidoreductase

Five times, 200 ml LB medium were treated with 100 μ g/ml carbenicillin and 100 μ M isopropyl β -D-thiogalactoside (IPTG), inoculated with in each case a colony of the strain MC4100 Δ mqo/pUCH2 and in each case cultured in 1 l conical flasks for 16 hours at 37°C and 200 revolutions per minute. The cells were washed twice in buffer A (50 mM hepes, 10 mM potassium acetate, 10 mM CaCl₂, 5 mM MgCl₂, adjusted to pH 7.5 with NaOH) at 4°C and resuspended in 40 ml of the same buffer. The cells were then broken down twice in a precooled French Pressure Cell from Spectronic Unicam

(Rochester, NY, USA) under 69 MPa (mega-Pascal). The cell debris was then sedimented twice in a centrifuge at 4°C for 10 minutes at 10000 x g. The supernatant was then centrifuged for 30 minutes at 75000 x g and 4°C. The
5 membrane pellet was resuspended with the same volume of buffer B (50 mM Na phosphate, 200 mM NaCl, pH 7.5) and centrifuged again for 30 minutes at 75000 x g and 4°C. The pellet was then resuspended with 1 ml buffer B. The histidine-tagged malate:quinone oxidoreductase protein was
10 purified in two steps.

Step 1: Solubilization:

2 % Triton X-100 and 10 % glycerol were added to the resuspended membranes and the batch was incubated for 10 minutes on ice. The batch was then centrifuged for 30
15 minutes at 200000 x g at 4°C.

Step 2: Affinity chromatography:

The equilibration of the "Talon-Metal-Affinity Resin" column material (500 µl column volume, CLONTECH Laboratories, Palo Alto, USA) was carried out twice with
20 1 ml buffer B and once with 1 ml buffer C (50 mM Na phosphate, 200 mM NaCl, 0.05 % Triton X-100, 10 µM flavin adenine dinucleotide (FAD), 0.2 mg/ml phospholipid, pH 7.0). The phospholipid used was L-α
phosphatidylethanolamine, type IX from E. coli (Sigma-
25 Aldrich, Deisenhofen, Germany), which was mixed as a 30 mg/ml stock solution in deionized water and treated briefly with an ultrasound apparatus (BRANSON Sonifier Cell Disrupter B15) for a few seconds until the suspension was transparent. The supernatant (1 ml) from step 1 was
30 applied to the equilibrated column and incubated for 20 minutes at room temperature. Thereafter, the column was flushed five times with buffer D (50 mM Na phosphate, 200 mM NaCl, 0.05 % Triton X-100, 10 % glycerol, 10 µM FAD, 0.2 mg/ml phospholipid, 10 mM imidazole, pH 7.0) and then

eluted twice with 500 μ l buffer E (50 mM Na phosphate, 200 mM NaCl, 0.05 % Triton X-100, 10 % glycerol, 10 μ M FAD, 0.2 mg/ml phospholipid, 100 mM imidazole, pH 7.0). The two fractions were combined and a buffer exchange was carried out by means of an ULTRAFREE-0.5 Centrifugal Filter Device (Millipore Corporation, Bedford, MA, USA), in order to remove the imidazole and to reduce the volume to 500 μ l. A second affinity chromatography was then carried out with the "Talon-Metal-Affinity Resin" column material (250 μ l column volume), as described above. The purified protein was stored at -20°C.

The purified malate:quinone oxidoreductase protein was investigated by means of SDS polyacrylamide gel electrophoresis and subsequent staining with Coomassie blue. In this analysis, two protein bands (protein B and protein C) with the mobility corresponding to a molecular weight of about 60 ± 2 KD (kilo-Dalton) were detected. The two proteins were blotted on to a polyvinylidene difluoride (PVDF) membrane (Boehringer Mannheim, Mannheim, Germany) and stained with Coomassie blue. The two protein bands were then cut out of the blot membrane.

Example 6

Determination of the N-position amino acid sequence

The N-position amino acid sequences of the malate:quinone oxidoreductase protein B and protein C were determined by Edman degradation (Edman, Molecular Biology Biochemistry Biophysics 8:211-55(1970)) by means of the automatic sequencer Procise Sequencer from PE Biosystems (Foster City, CA, USA). For protein B the amino acid sequence L N A V S M (see also SEQ ID No. 11) and for protein C the amino acid sequence A V S M A A K (see also SEQ ID No. 12) was determined.

Brief Description of the Figures:

Figure 1: Map of the plasmid pMW218mqo containing the mqo gene.

The length data are to be understood as approx. data. The
5 abbreviations and designations used have the following meaning:

- Plac: Promoter sequence of the lactose operon
- Kan: Kanamycin resistance gene

The abbreviations for the restriction enzymes have the
10 following meaning

- AccI: Restriction endonuclease from *Acinetobacter calcoaceticus*
- ClaI: Restriction endonuclease from *Caryophanon latum*
- EcoRI: Restriction endonuclease from *E. coli*
- 15 • KpnI: Restriction endonuclease from *Klebsiella pneumoniae*
- SalI: Restriction endonuclease from *Streptomyces albus*

What is claimed is:

1. A polypeptide from Enterobacteriaceae with
malate:quinone oxidoreductase (Mqo) activity (E.C.
1.1.99.16) chosen from the group consisting of
 - 5 a) polypeptide with the amino acid sequence shown in
SEQ ID NO. 2, or
 - b) polypeptide which is at least 70%, preferably at
least 80%, particularly preferably at least 90 to
95% identical to the amino acid sequence shown in
10 SEQ ID NO. 2, or
 - c) polypeptide according to SEQ ID NO. 2, including
deletion, insertion or exchange of one or more
amino acids, or
 - d) polypeptide according to SEQ ID NO. 2, including N-
15 or C-terminal lengthening by one or more amino
acids,

the total length of the polypeptide according to b), c)
or d) being at least 514 and at most 544, preferably at
least 519 and at most 539, in a preferred form at least
20 524 and at most 534, particularly preferably at least
527 and at most 531 amino acid radicals.
2. A polynucleotide from Enterobacteriaceae which codes
for a polypeptide with malate:quinone oxidoreductase
(Mqo) activity (E.C. 1.1.99.16), chosen from the group
25 consisting of
 - a) DNA which contains the nucleotide sequence
corresponding to nucleobases 7 to 1593 of SEQ ID
NO. 1, or
 - b) DNA according to a) corresponding to the
30 degeneration of the genetic code, or

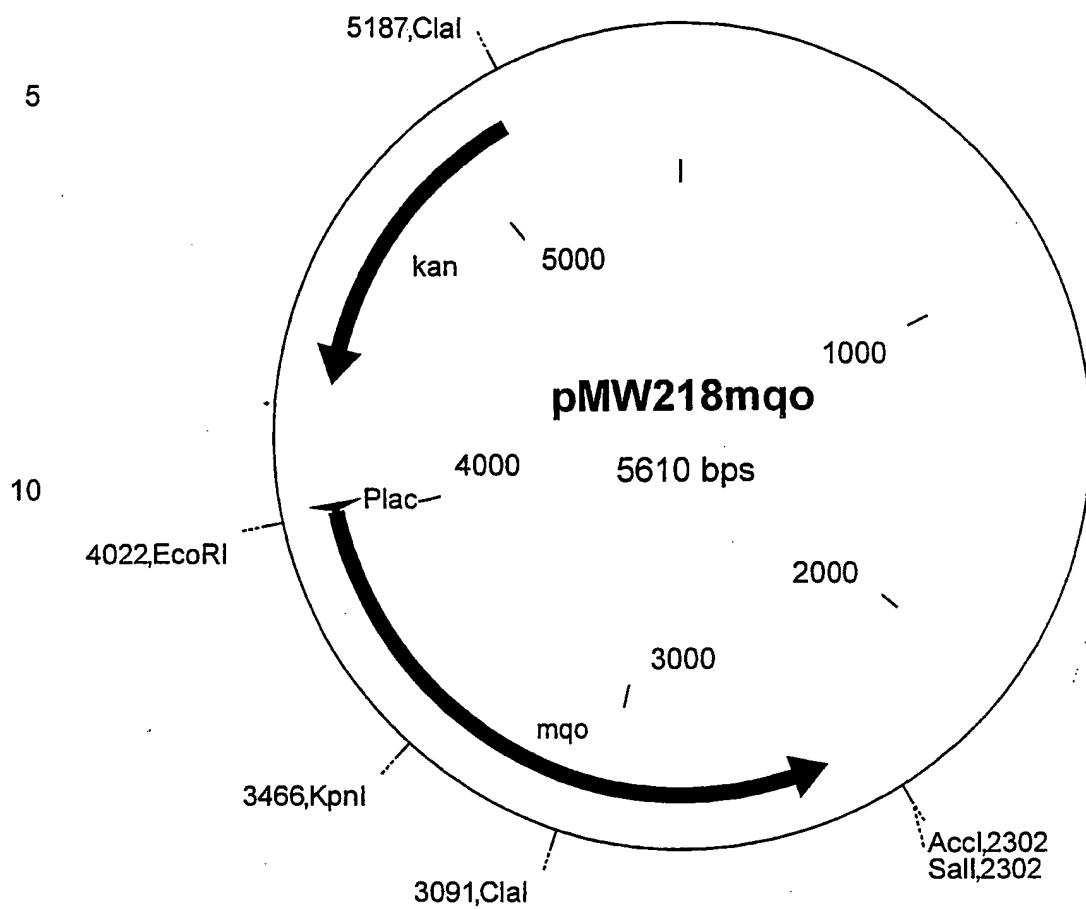
- c) DNA according to a) containing sense mutations of neutral function, or
 - d) DNA which is at least 70%, preferably at least 80%, particularly preferably at least 90 to 95% identical to that mentioned in a) or b), or
 - e) polynucleotide which hybridizes with the DNA according to a), b), c) or d).
3. A polynucleotide as claimed in claim 2, which is DNA which is capable of replication and codes for the polypeptide shown in SEQ ID NO. 2.
4. The plasmid pMW218mqo which contains the mqo gene of *Escherichia coli*.
5. A process for the fermentative preparation of L-threonine, which comprises employing Enterobacteriaceae bacteria, in particular those which already produce L-threonine and in which the nucleotide sequence(s) which code(s) for the mqo gene are enhanced, in particular over-expressed.
6. A process as claimed in claim 5, wherein further genes are enhanced in addition to the mqo gene.
7. A process as claimed in claim 5 or 6, wherein the microorganisms of the family Enterobacteriaceae are from the genus *Escherichia* and *Serratia*.
8. A process as claimed in claim 7, wherein the microorganisms are from the genus *Escherichia*, in particular of the species *Escherichia coli*.
9. A process as claimed in claim 5, wherein the thrABC operon which codes for aspartate kinase, homoserine dehydrogenase, homoserine kinase and threonine synthase is enhanced at the same time.

10. A process as claimed in claim 5, wherein the *pyc* gene which codes for pyruvate carboxylase is enhanced at the same time.
11. A process as claimed in claim 5, wherein the *pps* gene which codes for phosphoenol pyruvate synthase is enhanced at the same time.
12. A process as claimed in claim 5, wherein the *ppc* gene which codes for phosphoenol pyruvate carboxylase is enhanced at the same time.
- 10 13. A process as claimed in claim 5, wherein the genes *pntA* and *pntB* which code for transhydrogenase are enhanced at the same time.
14. A process as claimed in claim 5, wherein the gene *rhtB* which imparts homoserine resistance is enhanced at the same time.
- 15 15. A process as claimed in claim 5, wherein bacteria in which the metabolic pathways which reduce the formation of L-threonine are at least partly eliminated are employed.
- 20 16. A process as claimed in claim 5, wherein a strain transformed with a plasmid vector is employed and the plasmid vector carries the nucleotide sequence which codes for the *mgo* gene can be employed.
17. A process as claimed in claim 5, wherein bacteria transformed with the plasmid *pMW218mgo* are employed.
- 25 18. A process as claimed in claim 5, wherein the expression of the *mgo* gene is optionally induced with isopropyl β -D-thiogalactoside.
19. A process as claimed in claim 5, wherein at the same time the *gdhA* gene which codes for glutamate dehydrogenase is enhanced.
- 30

20. A process as claimed in claim 5, wherein at the same time the *rhtC* gene which imparts threonine resistance is enhanced.
21. A process as claimed in claim 5, wherein the nucleotide
5 sequence codes for a malate:quinone oxidoreductase protein with the N-terminal amino acid sequence Met Ala Ala Lys Ala Lys corresponding to SEQ ID No. 2.
22. A process as claimed in claim 5, wherein the nucleotide
10 sequence codes for a malate:quinone oxidoreductase protein with the N-terminal amino acid sequence Leu Asn Ala Val Ser Met according to SEQ ID no. 11.
23. A process as claimed in claim 5, wherein the nucleotide
15 sequence codes for a malate:quinone oxidoreductase protein with the N-terminal amino acid sequence Ala Val Ser Met Ala Ala Lys according to SEQ ID No. 12.
24. A process for the preparation of L-threonine, which comprises carrying out the following steps:
- a) fermentation of microorganisms of the family Enterobacteriaceae in which at least the *mqo* gene
20 is enhanced (over-expressed), optionally in combination with further genes,
 - b) concentration of the L-threonine in the medium or in the cells of the microorganisms of the family Enterobacteriaceae, and
 - 25 d[sic]) isolation of the L-threonine.
25. A malate-quinone oxidoreductase protein from Enterobacteriaceae with the N-terminal amino acid sequence according to SEQ ID No. 11.
26. A malate:quinone oxidoreductase protein from
30 Enterobacteriaceae with the N-terminal amino acid sequence according to SEQ ID No. 12.

27. An L-threonine-producing strain of the genus *Escherichia* with the genetic and phenotypic features of the strain B-3996kur Δ tdh/pVIC40, pMW218mqo.
28. The L-threonine-producing *Escherichia coli* strain B-3996kur Δ tdh/pVIC40, pMW218mqo deposited as.(sic) DSM 14004.

Figure 1:

 $\frac{1}{1}$ 

SEQUENCE PROTOCOL

<110> Degussa AG

5 <120> Process for the fermentative preparation of L-threonine.

<130> 000323 BT

<140>

10 <141>

<160> 12

<170> PatentIn Ver. 2.1

15

<210> 1

<211> 1720

<212> DNA

<213> Escherichia coli

20

<220>

<221> CDS

<222> (7)..(1593)

<223> mqo gene

25

<400> 1

```

aattcg atg gcg gca aaa gcg aaa gcg tcc gag gag cag gaa act gat      48
    Met Ala Ala Lys Ala Lys Ala Ser Glu Glu Gln Glu Thr Asp
          1             5             10

```

30

```

gta ctg ttg att ggc ggc ggc att atg agc gcc acg ttg ggg acc tat      96
Val Leu Leu Ile Gly Gly Gly Ile Met Ser Ala Thr Leu Gly Thr Tyr
    15             20             25             30

```

35

```

tta cgc gag ctg gag cct gaa tgg tcg atg acc atg gtg gag cgc ctg      144
Leu Arg Glu Leu Glu Pro Glu Trp Ser Met Thr Met Val Glu Arg Leu
          35             40             45

```

40

```

gag ggt gtc gcg cag gag agt tcg aac ggc tgg aat aac gcc gga acc      192
Glu Gly Val Ala Gln Glu Ser Ser Asn Gly Trp Asn Asn Ala Gly Thr
          50             55             60

```

45

```

ggg cat tct gca ctg atg gaa ctg aac tac acc ccg caa aac gcc gat      240
Gly His Ser Ala Leu Met Glu Leu Asn Tyr Thr Pro Gln Asn Ala Asp
          65             70             75

```

50

```

ggc agc atc agt att gaa aaa gca gtc gcc att aac gaa gca ttt cag      288
Gly Ser Ile Ser Ile Glu Lys Ala Val Ala Ile Asn Glu Ala Phe Gln
    80             85             90

```

```

att tcc cgc cag ttc tgg gcg cac cag gtt gag cgc ggc gtg ctg cgt      336
Ile Ser Arg Gln Phe Trp Ala His Gln Val Glu Arg Gly Val Leu Arg
    95             100             105             110

```

55

```

act ccg cgt tca ttt atc aat acc gtt ccg cat atg agc ttt gtc tgg      384
Thr Pro Arg Ser Phe Ile Asn Thr Val Pro His Met Ser Phe Val Trp
          115             120             125

```

60

```

ggc gag gat aac gtc aat ttc ctg cgc gcc cgt tac gcc gcg ttg caa      432
Gly Glu Asp Asn Val Asn Phe Leu Arg Ala Arg Tyr Ala Ala Leu Gln
          130             135             140

```

	caa agc tcg ctg ttt cgc ggt atg cgt tac tct gaa gat cac gcg cag	480
	Gln Ser Ser Leu Phe Arg Gly Met Arg Tyr Ser Glu Asp His Ala Gln	
	145 150 155	
5	atc aaa gag tgg gca ccg tta gtg atg gaa ggg cgc gat ccg caa cag	528
	Ile Lys Glu Trp Ala Pro Leu Val Met Glu Gly Arg Asp Pro Gln Gln	
	160 165 170	
10	aaa gtg gca gcc acg cgt acg gaa att ggt acc gat gtg aac tac ggc	576
	Lys Val Ala Ala Thr Arg Thr Glu Ile Gly Thr Asp Val Asn Tyr Gly	
	175 180 185 190	
15	gag atc acc cgc cag tta att gct tcc ttg cag aag aaa tct aac ttc	624
	Glu Ile Thr Arg Gln Leu Ile Ala Ser Leu Gln Lys Lys Ser Asn Phe	
	195 200 205	
20	tcg ctg caa ctc agc agc gaa gtc cgc gcc cta aag cgt aat gac gat	672
	Ser Leu Gln Leu Ser Ser Glu Val Arg Ala Leu Lys Arg Asn Asp Asp	
	210 215 220	
25	aac acc tgg acc gtt acc gtt gcc gat ctg aaa aat ggc act gca cag	720
	Asn Thr Trp Thr Val Thr Val Ala Asp Leu Lys Asn Gly Thr Ala Gln	
	225 230 235	
30	aac att cgt gcc aaa ttt gtc ttt atc ggc gcg ggc ggt gcg gcg ctg	768
	Asn Ile Arg Ala Lys Phe Val Phe Ile Gly Ala Gly Gly Ala Ala Leu	
	240 245 250	
35	aag ctg tta cag gaa tcg ggg att ccg gaa gcg aaa gac tac gcc ggt	816
	Lys Leu Leu Gln Glu Ser Gly Ile Pro Glu Ala Lys Asp Tyr Ala Gly	
	255 260 265 270	
40	ttc ccg gtg ggc gga cag ttc ctt gtt tcg gaa aac ccg gac gtg gtt	864
	Phe Pro Val Gly Gly Gln Phe Leu Val Ser Glu Asn Pro Asp Val Val	
	275 280 285	
45	aat cac cat ctg gcg aag gtt tac ggt aaa gca tcc gtt ggc gca cca	912
	Asn His His Leu Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro	
	290 295 300	
50	ccg atg tcg gtt ccg cat atc gat acc cgc gtt ctg gac ggt aaa cgc	960
	Pro Met Ser Val Pro His Ile Asp Thr Arg Val Leu Asp Gly Lys Arg	
	305 310 315	
55	gta gtg ctg ttt ggg cca ttt gcc acc ttc tca acc aaa ttc ctc aaa	1008
	Val Val Leu Phe Gly Pro Phe Ala Thr Phe Ser Thr Lys Phe Leu Lys	
	320 325 330	
60	aac ggt tca ttg tgg gat cta atg agt tcc acc acc acc tct aac gtg	1056
	Asn Gly Ser Leu Trp Asp Leu Met Ser Ser Thr Thr Thr Ser Asn Val	
	335 340 345 350	
65	atg ccg atg atg cac gtc ggg ctg gat aat ttc gat ctg gtg aaa tat	1104
	Met Pro Met Met His Val Gly Leu Asp Asn Phe Asp Leu Val Lys Tyr	
	355 360 365	
70	ctg gtg agt cag gtg atg ttg agt gaa gag gat cgt ttt gaa gcg ttg	1152
	Leu Val Ser Gln Val Met Leu Ser Glu Glu Asp Arg Phe Glu Ala Leu	
	370 375 380	

aaa gag tac tat ccg cag gcg aaa aaa gag gac tgg cgt ttg tgg caa 1200
 Lys Glu Tyr Tyr Pro Gln Ala Lys Lys Glu Asp Trp Arg Leu Trp Gln
 385 390 395

5 gcg ggg cag cgc gtg cag att atc aag cgt gat gcc gag aaa ggt ggc 1248
 Ala Gly Gln Arg Val Gln Ile Ile Lys Arg Asp Ala Glu Lys Gly Gly
 400 405 410

10 gta ctg cgt ctg ggt act gaa gtc gtc agt gac cag caa gga acc att 1296
 Val Leu Arg Leu Gly Thr Glu Val Val Ser Asp Gln Gln Gly Thr Ile
 415 420 425 430

15 gcc gcg ctc ctg ggg gca tcg cca ggg gcg tca acc gcc gcg ccg att 1344
 Ala Ala Leu Leu Gly Ala Ser Pro Gly Ala Ser Thr Ala Ala Pro Ile
 435 440 445

20 atg ttg aat ctg ctg gaa aaa gta ttt ggc gat cgt gtt tcc agc ccg 1392
 Met Leu Asn Leu Leu Glu Lys Val Phe Gly Asp Arg Val Ser Ser Pro
 450 455 460

caa tgg cag gct acg ttg aaa gcg atc gtt ccg tct tat gga cgc aag 1440
 Gln Trp Gln Ala Thr Leu Lys Ala Ile Val Pro Ser Tyr Gly Arg Lys
 465 470 475

25 ctg aac ggt gat gta gcg gca aca gaa cgc gag ttg cag tac acc agc 1488
 Leu Asn Gly Asp Val Ala Ala Thr Glu Arg Glu Leu Gln Tyr Thr Ser
 480 485 490

30 gaa gtg ctg ggg ttg aac tac gac aag ccg cag gca gca gat agt acg 1536
 Glu Val Leu Gly Leu Asn Tyr Asp Lys Pro Gln Ala Ala Asp Ser Thr
 495 500 505 510

35 ccg aaa ccg cag ttg aaa ccg caa ccc gtt caa aaa gaa gtg gcg gat 1584
 Pro Lys Pro Gln Leu Lys Pro Gln Pro Val Gln Lys Glu Val Ala Asp
 515 520 525

att gcg ttg taatgatacg ccacatccgg catggtatgc cggtatgtggc 1633
 Ile Ala Leu

40 gtatgctgat aagacgcgcc agcgtcgcat caggcaaccg gctcgggcgt tagatgttgg 1693
 atgcggcgta tcggggatcc tctagag 1720

45 <210> 2
 <211> 529
 <212> PRT
 <213> Escherichia coli

50 <400> 2
 Met Ala Ala Lys Ala Lys Ala Ser Glu Glu Gln Glu Thr Asp Val Leu
 1 5 10 15

55 Leu Ile Gly Gly Gly Ile Met Ser Ala Thr Leu Gly Thr Tyr Leu Arg
 20 25 30

Glu Leu Glu Pro Glu Trp Ser Met Thr Met Val Glu Arg Leu Glu Gly
 35 40 45

60 Val Ala Gln Glu Ser Ser Asn Gly Trp Asn Asn Ala Gly Thr Gly His
 50 55 60

Ser Ala Leu Met Glu Leu Asn Tyr Thr Pro Gln Asn Ala Asp Gly Ser

	65		70		75		80
	Ile Ser Ile Glu Lys	Ala Val Ala Ile Asn Glu Ala Phe Gln Ile Ser					
		85		90			95
5	Arg Gln Phe Trp	Ala His Gln Val Glu Arg Gly Val Leu Arg Thr Pro					
		100		105			110
10	Arg Ser Phe Ile Asn Thr Val Pro His Met Ser Phe Val Trp Gly Glu						
		115		120			125
	Asp Asn Val Asn Phe Leu Arg Ala Arg Tyr Ala Ala Leu Gln Gln Ser						
		130		135			140
15	Ser Leu Phe Arg Gly Met Arg Tyr Ser Glu Asp His Ala Gln Ile Lys						
		145		150			155
	Glu Trp Ala Pro Leu Val Met Glu Gly Arg Asp Pro Gln Gln Lys Val						
		165		170			175
20	Ala Ala Thr Arg Thr Glu Ile Gly Thr Asp Val Asn Tyr Gly Glu Ile						
		180		185			190
25	Thr Arg Gln Leu Ile Ala Ser Leu Gln Lys Lys Ser Asn Phe Ser Leu						
		195		200			205
	Gln Leu Ser Ser Glu Val Arg Ala Leu Lys Arg Asn Asp Asp Asn Thr						
		210		215			220
30	Trp Thr Val Thr Val Ala Asp Leu Lys Asn Gly Thr Ala Gln Asn Ile						
		225		230			235
	Arg Ala Lys Phe Val Phe Ile Gly Ala Gly Gly Ala Ala Leu Lys Leu						
		245		250			255
35	Leu Gln Glu Ser Gly Ile Pro Glu Ala Lys Asp Tyr Ala Gly Phe Pro						
		260		265			270
40	Val Gly Gly Gln Phe Leu Val Ser Glu Asn Pro Asp Val Val Asn His						
		275		280			285
	His Leu Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met						
		290		295			300
45	Ser Val Pro His Ile Asp Thr Arg Val Leu Asp Gly Lys Arg Val Val						
		305		310			315
	Leu Phe Gly Pro Phe Ala Thr Phe Ser Thr Lys Phe Leu Lys Asn Gly						
		325		330			335
50	Ser Leu Trp Asp Leu Met Ser Ser Thr Thr Thr Ser Asn Val Met Pro						
		340		345			350
55	Met Met His Val Gly Leu Asp Asn Phe Asp Leu Val Lys Tyr Leu Val						
		355		360			365
	Ser Gln Val Met Leu Ser Glu Glu Asp Arg Phe Glu Ala Leu Lys Glu						
		370		375			380
60	Tyr Tyr Pro Gln Ala Lys Lys Glu Asp Trp Arg Leu Trp Gln Ala Gly						
		385		390			395
	Gln Arg Val Gln Ile Ile Lys Arg Asp Ala Glu Lys Gly Gly Val Leu						

405 410 415
 Arg Leu Gly Thr Glu Val Val Ser Asp Gln Gln Gly Thr Ile Ala Ala
 420 425 430
 5 Leu Leu Gly Ala Ser Pro Gly Ala Ser Thr Ala Ala Pro Ile Met Leu
 435 440 445
 10 Asn Leu Leu Glu Lys Val Phe Gly Asp Arg Val Ser Ser Pro Gln Trp
 450 455 460
 Gln Ala Thr Leu Lys Ala Ile Val Pro Ser Tyr Gly Arg Lys Leu Asn
 465 470 475 480
 15 Gly Asp Val Ala Ala Thr Glu Arg Glu Leu Gln Tyr Thr Ser Glu Val
 485 490 495
 Leu Gly Leu Asn Tyr Asp Lys Pro Gln Ala Ala Asp Ser Thr Pro Lys
 500 505 510
 20 Pro Gln Leu Lys Pro Gln Pro Val Gln Lys Glu Val Ala Asp Ile Ala
 515 520 525
 Leu
 25
 30 <210> 3
 <211> 25
 <212> DNA
 <213> Artificial sequence
 35 <220>
 <223> Description of the artificial sequence: Primer YojH1
 <400> 3
 gcggaattcg atggcggcaa aagcg 25
 40 <210> 4
 <211> 20
 <212> DNA
 <213> Artificial sequence
 45 <220>
 <223> Description of the artificial sequence: Primer YojH2
 <400> 4
 50 gttacgccgc atccaacatc 20
 <210> 5
 <211> 20
 55 <212> DNA
 <213> Artificial sequence
 <220>
 <223> Description of the artificial sequence: Primer Tdh1
 60 <400> 5
 tcgcgaccta taagtttggg 20

<210> 6
<211> 20
<212> DNA
5 <213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer Tdh2
10 <400> 6
aataccagcc cttgttcgtg 20

<210> 7
15 <211> 24
<212> DNA
<213> Artificial sequence

<220>
20 <223> Description of the artificial sequence: Primer
YOJH1a

<400> 7
25 ggatccgttg atgccgcgca aatc 24

<210> 8
<211> 48
<212> DNA
30 <213> Artificial sequence

<220>
<223> Description of the artificial sequence: Primer YCHIS
35 <400> 8
cgcgaaattct tagtggtggt ggtggtggtg caacgcaata tccgccac 48

<210> 9
40 <211> 20
<212> DNA
<213> Artificial sequence

<220>
45 <223> Description of the artificial sequence: Primer Y_01

<400> 9
gctggatgaa tgggcggcgg 20

50
<210> 10
<211> 27
<212> DNA
<213> Artificial sequence
55
<220>
<223> Description of the artificial sequence: Primer Y_04

<400> 10
60 cgcggatccc cggtttcaac gatgatg 27

<210> 11

7

- <211> 6
<212> PRT
<213> Escherichia coli
- 5 <220>
<223> N-Terminus of the malate:quinone oxidoreductase
protein B.
- <400> 11
10 Leu Asn Ala Val Ser Met
1 5
- 15 <210> 12
<211> 7
<212> PRT
<213> Escherichia coli
- 20 <220>
<223> N-Terminus of the malate:quinone oxidoreductase
protein C.
- <400> 12
25 Ala Val Ser Met Ala Ala Lys
1 5

30

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 01/05548

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N9/02 C12P13/08 C12N15/53

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N C12P

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

BIOSIS, WPI Data, PAJ, EPO-Internal, EMBL, EMBASE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	KATHER BIRGIT. ET AL: "Another unusual type of citric acid cycle enzyme in Helicobacter pylori: The malate:quinone oxidoreductase." JOURNAL OF BACTERIOLOGY, vol. 182, no. 11, June 2000 (2000-06), pages 3204-3209, XP002179952 ISSN: 0021-9193	1-4, 25, 26
Y	tables 1,2	5-24, 27, 28
X	DATABASE EMBL 'Online! BLATTNER F.R. ET AL.: "The complete genome sequence of Escherichia coli K-12." retrieved from EBI Database accession no. P33940 XP002179954 the whole document	1-4, 25, 26

-/-



Further documents are listed in the continuation of box C.



Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
- *L* document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)
- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
- *X* document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *Z* document member of the same patent family

Date of the actual completion of the international search

19 October 2001

Date of mailing of the international search report

05/11/2001

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax (+31-70) 340-3016

Authorized officer

Lanzrein, M

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 01/05548

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT		
Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	DE 198 31 609 A (KERNFORSCHUNGSANLAGE JUELICH) 15 April 1999 (1999-04-15) page 5, line 55 -page 6, line 10	5-24
Y	EP 0 436 886 A (KERNFORSCHUNGSANLAGE JUELICH) 17 July 1991 (1991-07-17) the whole document	6-14, 19, 20
Y	US 5 939 307 A (LIAW HUNGMIN JAMES ET AL) 17 August 1999 (1999-08-17) column 7, line 42-57; claims 4, 17-20	27, 28
A	MOLENAAR D ET AL: "BIOCHEMICAL AND GENETIC CHARACTERIZATION OF THE MEMBRANE-ASSOCIATED MALATE DEHYDROGENASE (ACCEPTOR) FROM CORYNEBACTERIUM GLUTAMICUM" EUROPEAN JOURNAL OF BIOCHEMISTRY, BERLIN, DE, vol. 254, 1998, pages 395-403, XP000941422 ISSN: 0014-2956 the whole document	1-28
A	VOGEL R F ET AL: "CLONING AND SEQUENCE OF THE MDH STRUCTURAL GENE OF ESCHERICHIA COLI CODING FOR MALATE DEHYDROGENASE" ARCHIVES OF MICROBIOLOGY, BERLIN, DE, vol. 149, 1987, pages 36-42, XP002932511 ISSN: 0302-8933 the whole document	1-28
P, X	VAN DER REST MICHEL E ET AL: "Functions of the membrane-associated and cytoplasmic malate dehydrogenases in the citric acid cycle of Escherichia coli." JOURNAL OF BACTERIOLOGY, vol. 182, no. 24, December 2000 (2000-12), pages 6892-6899, XP002179953 ISSN: 0021-9193 the whole document	1-4, 25-28
P, Y	EP 1 038 969 A (DEGUSSA) 27 September 2000 (2000-09-27) the whole document	1-28
P, Y	EP 1 085 091 A (DEGUSSA ; KERNFORSCHUNGSANLAGE JUELICH (DE)) 21 March 2001 (2001-03-21) the whole document	1-28

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 01/05548

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
DE 19831609	A	15-04-1999	DE 19831609 A1	15-04-1999
			AU 1148299 A	27-04-1999
			BR 9813021 A	15-08-2000
			CN 1275167 T	29-11-2000
			WO 9918228 A2	15-04-1999
			EP 1015621 A2	05-07-2000
			HU 0004381 A2	28-03-2001
			SK 4812000 A3	12-09-2000
EP 0436886	A	17-07-1991	DE 3942947 A1	27-06-1991
			DE 59005821 D1	30-06-1994
			EP 0436886 A1	17-07-1991
US 5939307	A	17-08-1999	AU 730102 B2	22-02-2001
			AU 3899497 A	20-02-1998
			BR 9710503 A	11-01-2000
			CN 1226931 A	25-08-1999
			EP 0917578 A1	26-05-1999
			HU 9903856 A2	28-03-2000
			JP 2000515763 T	28-11-2000
			NO 990362 A	26-01-1999
			PL 331351 A1	05-07-1999
			TR 9900213 T2	21-04-1999
			WO 9804715 A1	05-02-1998
EP 1038969	A	27-09-2000	DE 19912384 A1	21-09-2000
			AU 2236900 A	21-09-2000
			BR 0001342 A	02-05-2001
			CN 1267734 A	27-09-2000
			EP 1038969 A2	27-09-2000
			JP 2000270888 A	03-10-2000
			SK 3742000 A3	09-10-2000
EP 1085091	A	21-03-2001	DE 19941478 A1	08-03-2001
			CN 1291651 A	18-04-2001
			EP 1085091 A1	21-03-2001
			JP 2001095592 A	10-04-2001